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```

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
192 CCGGTGCTGGATATCTCCGCCGAGACTTTTTAGCTGGCTTAGCATCA 241

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
175 pArGtYrPhePrIleAlaSerValMetArGThrLeuAspLysAspAsn 192

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
242 CAGAGTTTTTCACCTACTACTAGTAGTGACGACACGGCTCGGATCCTCT 291

|||.....:|||||.....:|||||.....:|||||.....:|||||.....:
192 heSeRLeuthrProaspLeuIlleHisAspLeuLeuGlYHisValProtp 208

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
292 ACACCCAGAACCCGATACATGCCATGAACTTTGGGACATGTGCCTCTA 341

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
209 LeuLeuHIsProSerPheSerclupPhePHeIleAsnMetGLyArgLeuPh 225

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
342 CTGTGTCATCCTTAAGTTTGCCAGTTTTCACAAGAGATAGGA..... 383

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
225 eThrlySValIlleGlulYSValgluAlaLeuProSerLYSLysGLInArgI 242

|||||.....:CTGCCTCATTTGGGACATCTGACGAAGATG 414

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
42 leclnThrLeuglnSerAsnLeuIlleAlaIleValArgcysPheTrpPhe 258

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
415 TTCAGAANATTGACCAT.....:TGCTATTTTTT 443

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
259 ThrValgluSerGlyLeuileGluasnHisGluGlyArgLyAlaTyrgl 275

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
444 AGCATTTGAATTTGGCTTTTTCGAAAGGAAGGACACTAGTGCCTTTATGG 493

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
275 yAlaValLeuilleSerSerProGlnGluLeuGlyHisAlaPheIleAspa 292

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
494 GGCAGACACTCTGCTCTCTATTGGAGAACTAAAGCAGTCTCTTCTCGACA 543

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292 snValArgVallLeuProLeuGluLeuAspGlnlleIleArgLeuProPhe 593

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
544 AGGCCAAGGTGAAAAACATTTCGATCCGAAGACAACCTGTTTGCAGAAGTGC 632

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
309 AsnThrSerThrProGlnGluThrLeuPheSerIleAargHisPheaspGI 325

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
594 CTTATCACCACTTTTCAGGAAGCTTACTTTGTTTCAGAAAAGTTNTGAAGA 643

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
325 uLeuValGlu 328

|||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
644 AGCCAAAGAA 653

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seq_name: qb_est14:AA968411

seq=documentation_block:
 LC AA968411 669 bp mRNA EST 20-MAY-1998
 DESCRIPTION gb|U05.v1 Sugano mouse liver mlia Mus musculus cDNA clone
 IMAGE|1431057.5 similar to gb|K03020 PHENYLALANINE-4-HYDROXYLASE
 (HUMAN); gb|X51942 Mouse mRNA for phenylalanine hydroxylase (MOUSE
); mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS

TITLE

THE JOURNAL

COMMENT

WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

```

this clone is available royally-free through LILNI; contact the
IMAGE Consortium (info@image.lilni.gov) for further information.
MGI:915125
Seq primer: primer name ambiguous
High quality sequence stop: 465.
Location/Qualifiers
    1. .669
       /organism="Mus musculus"
       /strain="C57BL"
       /db_xref="taxon:10090"
       /clone="IMAGE:1431057"
       /clone_lib="Sugano mouse liver mlia"
       /sex="female"
       /dev_stage="adult"
       /lab_host="DH10B"
       /note="Organ: liver; Vector: pME18S-FL3; Site.1: DraIII
(CACTGTG); Site.2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTCGCCCTTTTCTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTCGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTG, 3' site CACCATGTG). xhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCCTGCTCTTAAGCTGCG and 3' end
primer CGACCTGCGAGCTCGACACA."
165 c 158 g 204 t
142 a

```

BASE COUNT	142 a	165 c	158 g	204 t
ORIGIN				

alignment_scores:		
Quality:	211.00	Length: 189
Ratio:	1.936	Gaps: 4
Percent Similarity:	57.672	Percent Identity: 30.688

alignment block:

US-09-438-185-1047 x AA968411
alignment_block:

align seq 1/1 to: AA968411 from: 1 to: 669

[illegible]

247 erAsnLeuileAlaileValargCysPheThrValGluSerGly 263
 :::::::::::::::ATTACTGCTTTACTGTGGAGTTGGG 384
 356 CA.....
 264 LeuileGluAsnHisGluGlyAlaGlyAlaGlyAlaValLeuileSe 280
 :::::::::::::::TTTAAAGGCATATGGTGGCTGGCTGTGTC 434
 385 CTTTGAAGCAAGAGAGATTCTATAAGGCATATGGTGGCTGGCTGTGTC 434
 280 rSerProGlnGluLeuGlyHisAlaPheIleAsnValargValLeuP 297
 :::::::::::::::TTTATCAGACAGCAAGCAAGCTCTGC 484
 435 ATCCTTTGGAGATTACAGTACTGTTTATCAGACAGCAAGCAAGCTCTGC 484
 297 rLeuGluLeuAspGln 302
 :::::::::::::::
 485 CCCTGGAGCTAGAGAG 501

seq_name: gb_est40:AV650135

seq_documentation_block: 607 bp mRNA EST 07-SEP-2000
 LOCUS AV650135 GLC Homo sapiens cDNA clone GLCCBF06 3', mRNA sequence.
 DEFINITION AV650135
 VERSION AV650135.1 GI:98711149
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 607)
 AUTHORS Qian, B., Wu, T., Huang, Q., Kang, B., Gao, X., Xu, Z., Xiao, H.,
 Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Qu, J.,
 Zeng, L., Xu, S., Gu, M., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu,
 G., Yang, Y., Gu, Y., Chen, Z., and Han, Z.
 TITLE Homo sapiens cDNA clone
 JOURNAL Unpublished (2000)
 COMMENT Contact: Zengqiang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203 P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzeng@sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 source

1..607
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GLCCBF06"
 /clone_lib="GLC"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI."
 BASE COUNT 143 a 162 c 138 g 163 t 1 others
 ORIGIN

alignment_scores:
 Quality: 210.50 Length: 207
 Ratio: 1.784 Gaps: 4
 Percent Similarity: 57.005 Percent Identity: 28.502

alignment_block:

US-09-438-185-1047 x AV650135

Align seg 1/1 to: AV650135 from: 1 to: 607

104 ArgAsnLeuThrTrpTyArgLeuLeuSerSerArgPheSerLeuTrpLysSe 120
 :::::::::::::::
 34 AAGAAACATGGGCACAGATTCTCAAGACTCTGAAGTCTGTGTATAAAC 83

120 rTyCysProArgPheLeuAspTyTrLeuGluAlaPheGlyLeuLeus 137
 :::::::::::::::TGCTATGAGTACAATCACATTTTCCACTTCTTG 124
 84 CCATGCT.....
 137 erAspPheLeuAspHis.....GlnAlaVal 145
 :::::::::::::::
 125 AAAAGTACTGTGCTTCCATGAAGATAAATCCCCAGCTGGAAGAGCTT 174
 146 ILySPhePheGluLeuGluThrHisPheSerTyTyTrProValSerG1 162
 :::::::::::::::TTTCCGCTCCGACCTGTAGCTGG 224
 175 TCTCAGTTCTCGCAGACTTGCCTGCTTCCGCTCCGACCTGTAGCTGG 224
 162 yPheValAlaProHisGlnTyTrLeuSerLeuGlnAspArgTyPheP 179
 :::::::::::::::TTTGGTGGCTTCCGCTTCCGAGTCTTCC 274
 225 CCHGCTTCTCTGGGATTTCTGGTGGCTTCCGCTTCCGAGTCTTCC 274
 179 rolleAlaSerValMetArgThrLeuAspLysAspAsnPheSerLeuThr 195
 :::::::::::::::TTTCCAGGAAATTTGGC..... 405
 275 ACTGCACACAGTACATCAGACATGGATGCAAGCCCATATATACCCCGAA 324
 196 ProAspLeuIleHisAspLeuGlyHisValProTrpLeuLeuHisPr 212
 :::::::::::::::TTTGGGACATGTGCCCTTGTTCAGATCG 374
 325 CTTGACATCTGCCATGAGCTGTGGGACATGTGCCCTTGTTCAGATCG 374
 212 oSerPheSerGluPhePheIleAsnMetGlyArgLeuPheThrLysValI 229
 :::::::::::::::
 375 CAGCTTTGCCAGCTTTTCCAGGAAATTTGGC..... 405
 229 leGluLysValGlnAlaLeuProSerLysLysGlnArgIleGlnThrLeu 245
 :::::::::::::::CTTGCTCTCTGGTGGCACCCTGATGATACATTTGAAAGCTC 447
 406CTTGCTCTCTGGTGGCACCCTGATGATACATTTGAAAGCTC 447
 246 GlnSerAsnLeuIleAlaIleValArgCysPheTrpPheThrValGluSe 262
 :::::::::::::::ATTACTGGTTTACTGTGGAGTT 476
 448 GCCACA.....
 262 rGlyLeuIleGluAsnHisGluGlyArgLysAlaTyGlyAlaValLeuI 279
 :::::::::::::::TTTGGCTCTCAACANGGACCTCCATAAGGCATATGTGCTGGCTCC 526
 477 TGGCTCTCAACANGGACCTCCATAAGGCATATGTGCTGGCTCC 526
 279 leSerSerProGlnGluLeuGlyHisAlaPheIleAspAsnValArgVal 295
 :::::::::::::::
 527 TGTATCTCTTGTGTAATACACTACTGCTTATCAGAGAAAGCAAGCTT 576
 296 LeuProLeuGluLeuAspGln 302
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 577 CTCCTCCCTGGAGCTGGAGAG 597

seq_name: gb_est103:C93903

seq_documentation_block:
 LOCUS C93903 729 bp mRNA EST 08-JUN-1998
 DEFINITION C93903 Dictyostelium discoideum SS (M.Yoshida) Dictyostelium
 discoideum cDNA clone SSL848, mRNA sequence.
 ACCESSION C93903
 VERSION C93903.1 GI:3192312
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum.
 ORGANISM Dictyostelium discoideum.
 Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 REFERENCE 1 (bases 1 to 729)
 AUTHORS Yoshida, M.
 TITLE Developmental cDNA in Dictyostelium discoideum (M.Yoshida)
 JOURNAL Unpublished (1998)
 COMMENT Contact: Motonobu Yoshida
 Research Institute of Food Science
 Kinki University
 Nakamachi 3327, Nara 631, Japan
 Email: yoshida@ws06.nara.kindai.ac.jp
 Dictyostelium discoideum cDNA project in Japan.
 Location/Qualifiers
 1..729
 /organism="Dictyostelium discoideum"

us-09-438-185-1047.rst

Thu Jul 5 11:24:06 2001

366 AACCAAAATACCAATTAAT.....CCATT 394

309 AsnThrSerThrProGlnGluThrLeuPheSerIleArg.HisPheAspG 325

395 GACGATGCACTACTGAATATCCAAATTCACCAATTCACCACTTTACTA 444

325 luLeuValGluLeuThrSerLysLeuGluTrpMetLeuAspGlnGlyLeu 341

445 TGTTGCAGAAAGTTTCCAAAAGCAAAAGCAAAATGAGCAATTTGCTG 494

342 LeuGlu.....SerIleProLeuThrAsnG 350

495 ATAGCTTTAAAAAACCAATTTCAATTCGTTACATCCATACACTCAATCA 544

350 nGluLysThrLeu 354

545 ATTGAATACTTG 557

seq_name: gb_est100:BG429401

seq_documentation_block: 674 bp mRNA EST 14-MAR-2001
LOCUS BG429401 602499620F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613404 5',
DEFINITION mRNA sequence.

ACCESSION BG429401 GI:13335907

VERSION BG429401.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 674)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1995)

Contact: Robert Strausberg, Ph.D.

Email: cgaab@rmail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: L1CM1363 row: 9 column: 05

High quality sequence stop: 665.

Location/Qualifiers

1..674

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NIH_MGC_75"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: kidney; Vector: pBR-LIB (Clontech); Site_1:

SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGAGCGCCGACATG-dt(30)BN-3 (where B = A, 65

Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.

1 (bases 1 to 653)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,

Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, I.

The Dictyostelium developmental cDNA project: generation and

analysis of expressed sequence tags from the first-finger stage of

development

DNA Res. 5 (6), 335-340 (1998)

98156227

Contact: Hideko Urushihara

Institute of Biological Sciences

University of Tsukuba

3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan

Email: d402hu@sakura.cc.tsukuba.ac.jp

PROJECT - "Dictyostelium discoideum cDNA project in Japan"

POLYA-No. Location/Qualifiers

1..653

/organism="Dictyostelium discoideum"

/strain="AX4"

/db_xref="taxon:44689"

/clone_lib="SSM681"

/dev_stage="slug"

231 a 107 c 98 g 217 t

BASE COUNT 231 a 107 c 98 g 217 t

ORIGIN

alignment_scores:

Quality: 204.50 Length: 205

Ratio: 1.763 Gaps: 5

Percent Similarity: 56.585 Percent Identity: 28.293

alignment_block:

US-09-438-185-1047 x C93147

Align seg 1/1 to: C93147 from: 1 to: 653

159 ProValSerGlyPheValAlaProHisGlnTrpLeuSerLeuGlnAs 175

14 CCAGTACAAGTTTACTCTCGTAGAGATTCTTAATGGTTAGCTTT 63

175 pArgTrpProIleAlaSerValMetArgThrLeuAspLysAspAsn 192

64 CCGTGTATCCACTCACTCAATATATTAGACATCCATCCGATCAT 113

192 heserLeuThrProAspLeuIleHisAspLeuGlyHisValProTrp 208

114 ATACACCAACAGATGTTCTGTCATGAATTATTAGTTCATGTTCCAT 163

209 LeuLeuHisProSerPheSerGluPhePheIleAsnMetGlyArgLeuPh 225

164 TTACGTCATCCGATTCCTGCTCATTTTAGTCAAGAGATTGGT 205

225 eThrLysValIleGluLysValGlnAlaLeuProSerLysLysGlnArg 242

206TTAGCTTCATTTGGTCTCTGTATGAAGATA 236

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

alignment_scores:

Quality: 203.00 Length: 184

Ratio: 1.897 Gaps: 2

Percent Similarity: 58.152 Percent Identity: 29.348

alignment_block:

BASE COUNT 160 a 181 c 155 g 177 t

ORIGIN

us-09-438-185-1047.rst

Thu Jul 5 11:24:06 2001

US-09-438-185-1047 x BG429401

Align seg 1/1 to: BG429401 from: 1 to: 674

145 ValLeuLysPheGluLeuLthrHisPheSerTyTyProValSe 161
 37 GTTCTCAGTCTCGGACCTGACATGCTGTTCCGCTCGACCTAGC 86
 161 rGlyPheValAlaProHisGlnTyLeuSerLeuGlnAspArgTyP 178
 87 TGGCTCTCTCTCGGATTCCTGGGTGCTGCTGCTGCTGCTGCT 136
 178 heProLleAlaSerValMetArgThrLeuAspLysAspAsnPheserLeu 194
 137 TCCACTGCACACAGTACATGATGATGATGATGATGATGATGAT 186
 195 ThrProAspLeuLleHisAspLeuLysGlnHisValProTrpLeuLthr 211
 187 CAACCTGACATCTGCCATGAGCTGTTGGGACATGTCGCTGTTT 236
 211 sProSerPheSerGluPhePheLeuAsnMetGlyArgLeuPheThrLys 228
 237 TGCAGCTTTCGCCAGTTTCCAGGAAATTGGC..... 270
 228 alileGluLysValGlnAlaLeuProSerLysLysGlnArgLleGlnThr 244
 271CTTGCCTCTCTGGTGCACCTGATGATGATGATGATG 309
 245 LeuGlnSerAsnLeuLleAlaLeuValArgCysPheTrpPheThrValG 261
 310 CTGCGCCACA.....ATTACTGTTTACTGTTGGA 338
 261 uSerGlyLeuLleGluAsnHisGluGlyArgLysAlaValLle 278
 339 GTTGGCTCTGCAACAGAGACTCTCAATAGGCATATGCTGCTGGC 388
 278 euLleSerSerProGlnGluLeuGlyHisAlaPheLleAspAsnValArg 294
 389 TCTCTGTCATCTTGGTGAATACAGTACTGCTTATCAGAGACCAAG 438
 295 ValLeuProLeuGluLeuAspGlnLleLeuArgLeuProPheAsnThrSe 311
 439 CTCTCTCCCTCGAGCTGAGAGACAGCCATCCAAATATACATGTCAC 488
 311 rThrProGlnGluLthrLeuPheSerLleArgHisPheAspGluLeuValG 328
 489 GGAGTTCACAGCCCTGATTACGTGCGACAGAGATTTAATGATGCAAGG 538
 328 lu 328
 539 AG 540

seq_name: gb_est40:AV651521

seq_documentation_block: 658 bp mRNA EST 07-SEP-2000
 LOCUS AV651521 GLC Homo sapiens cDNA clone GLCCOF11 3', mRNA sequence.
 DEFINITION AV651521
 ACCESSION AV651521
 VERSION AV651521.1 GI:9872535
 KEYWORDS EST:
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Qian,B., Wu,T., Huang,Q., Kang,B., Gao,X., Xu,Z., Xiao,H.
 Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Ou,J.,
 Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
 G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
 TITLE Homo sapiens cDNA clone
 JOURNAL Unpublished (2000)
 CONTACT: Zequang Han
 COMMENT Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzgechgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 source

1. 658
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GLCCOF11"
 /clone_lib="GLC"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 152 a 179 c 151 g 176 t
 ORIGIN

alignment_scores:
 Quality: 201.00 Length: 182
 Ratio: 1.896 Gaps: 2
 Percent Similarity: 58.242 Percent Identity: 29.121

alignment_block:

US-09-438-185-1047 x AV651521

Align seg 1/1 to: AV651521 from: 1 to: 658

147 LysPheGluLeuLthrHisPheSerTyTyProValSerGlyP 163
 6 CAGTTCCTCAGACTTGCACCTGTTCCGCTCCGACCTGAGTGGCCT 55
 163 eValAlaProHisGlnTyLeuSerLeuLleAspArgTyPheProI 180
 56 GCTTCTCTCTCGGATTCCTGGGTGCTGCTGCTGCTGCTGCT 105
 180 leAlaSerValMetArgThrLeuAspLysAspAsnPheserLeuThrPro 196
 106 GCACACAGTACATGACATGATGATGATGATGATGATGATGAT 155
 197 AspLeuLleHisAspLeuLysGlnHisValProTrpLeuLthrHisProSe 213
 156 GACATCTGCATGAGCTGTTGGACATGTCGCTGTTTTCAGATCGCAG 205
 213 rPheSerGluPhePheLleAsnMetGlyArgLeuPheThrLysValLleG 230
 206 CTTTGGCCAGTTTCCAGGAAATTGGC..... 233
 230 lylsValGlnAlaLeuProSerLysLysGlnArgLleGlnThrLeuGln 246
 234CTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 278
 247 SerAsnLeuLleAlaLeuValArgCysPheTrpPheThrValLleSerG 263
 279 ACA.....ATTACTGTTTACTGTTGAGTTGG 307
 263 yLeuLleGluAsnHisGluGlyArgLysAlaTyGlyAlaValLeuLle 280
 308 GCTCTGCAACAGGAGACTCCATAGAGGCAATGCTGCTGCTGCTG 357
 280 erSerProGlnGluLeuGlyHisAlaPheLleAspAsnValArgValLeu 296
 358 CATCTTTGGTGAATACAGTACTGCTTATCAGAGAGCCAAAGCTTCT 407
 297 ProLeuGluLeuAspGlnLleLeuArgLeuProPheAsnThrSerThrPr 313
 408 CCCCTGGAGCTGGAGAGAGACAGCCATCCAAATATACACTGTCACG 457
 313 oGlnGluLthrLeuPheSerLleArgHisPheAspGluLeuValGlu 328

458 CCACCCCTGTTACTGCGACAGAGTTTATGATGCAAGGAG 503

seq_name: gb_est15:AI056867

seq_documentation_block: 734 bp mRNA EST 29-SEP-1998
LOCUS AI056867
clone IMAGE:1674274 3' similar to gb:K03020
PHENYLALANINE-4-HYDROXYLASE (HUMAN);, mRNA sequence.

ACCESSION AI056867
VERSION AI056867.1 GI:3330656

KEYWORDS EST
SOURCE human

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 734)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

UNPUBLISHED (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-f@mail.nih.gov

This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 789 Std Error: 0.00
Seq primer: -40m3 fwd RT from Amersham

High quality sequence stop: 322.
Location/Qualifiers

1. 734
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1674274"
/sex="male"

/dev-stage="20 week-post conception fetus"
/lab-host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)"
with a modified polylinker; Site:1: Pac I; Site:2: Eco RI;
This is a subcloned version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AAGTGAAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 185 a 156 c 191 g 202 t

ORIGIN

alignment_scores:
Quality: 201.00 Length: 189
Ratio: 1.844 Gaps: 4
Percent Similarity: 57.672 Percent Identity: 29.630

alignment_block:

US-09-438-185-1047 x AI056867/rev

Align seg 1/1 to reverse of: AI056867 from: 1 to: 734

115 PheSerLeuThrLysSerTyrCysProArgPhePheLeuAspTyrLeuG1 131

599 TTTCACCTCTTGTGAAGAGTACTGT..... 576

131 uAlaPheGlyLeuSerAspPheLeuAspHis...GlnAlaValIleL 147

575GCCTCCATGAAGATACATCCCGACGCTGGAGACCTTTCTC 533

147 ySpPheGlyLeuLeuThrHisPheSerTyrTyrProValSerGlyPhe 163

532 AGTCTGCGAGCTGCTGCTTTCCGCTCCGACCTGCTAGCTGGCCTG 483

164 ValAlaProHisGlnTyrLeuSerLeuLeuGlnAspArgTyrPheProI1 180

482 CTTTCCCTCTCGGAGTTCTTGGTGGCTTGCCTTCGAGCTTCCACTG 433

180 eAlaSerValMetArgThrLeuAspLysAspSerLeuThrProA 197

432 CACACAGTACATACATGATCCACAGCCCATGTATACCCCGAACCTG 383

197 sPLeuIleHisAspLeuGlyHisValProTyrPheLeuHisProSer 213

382 ACATTTGCGATGAGCTGTGGACATGTGCTTTTCAGATCGCAGC 333

214 PheSerGluPhePheIleAsnMetGlyArgLeuPheThrLysValIleG1 230

332 TTTGCCAGCTTTTCCAGGAATTTGCC..... 306

230 uLysValGlnAlaLeuProSerLysLysGlnArgIleGlnThrLeuGlnS 247

305CTTGCTCTCTGGGTGCACCTGATGAATCCATTTGAAAGCTC.... 264

247 eAsnLeuIleAlaIleValArgCysPheThrPheThrValGluSerGly 263

263GCCCAATTTACTGCTTACTCTGAGTTGGG 231

264 LeuIleGluAsnHisGluGlyArgLysAlaTyrGlyAlaValLeuIleSe 280

230 CTTGCAACACAGGAGCTCCATTAAGGATATGCTGGCTGCTCTGTC 181

280 rSerProGlnGluLeuGlyHisAlaPheIleAspAsnValArgValLeup 297

180 ATCCTTTGGTGAATTCAGTACTGCTTTATCAGAGACCAAGCTTCTCC 131

297 roLeuGluLeuAspGln 302

130 CCTGGAGCTGGAGAG 114

seq_name: gb_est40:AV652188

seq_documentation_block: 642 bp mRNA EST 07-SEP-2000

LOCUS AV652188

DEFINITION AV652188 GIC Homo sapiens cDNA clone GLCCXG04 3', mRNA sequence.

ACCESSION AV652188

VERSION AV652188.1 GI:9873202

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 642)

Qian, B., Wu, T., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,

Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Qu, J.,

Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu

G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.

Homo sapiens cDNA clone

Unpublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1. 642

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="GLCCXG04"

/clone_lib="GIC"

/tissue_type="corresponding non cancerous liver tissue"

/dev_stage="Adult"

/lab_host="SOLR"

FEATURES

source

us-09-438-185-1047.rst

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1050)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue procurement: Jeffrey E. Green, M.D.
cDNA library preparation: Life Technologies, Inc.
cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9857 row: n column: 13
High quality sequence stop: 717.
Location/Qualifiers

FEATURES

source

1.1050

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="IMAGE:4241484"

/clone_lib="NCI CGAP Kid14"

/lab_host="DH10B (T1 phage-resistant)"

Note: Organ: kidney; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library. |"

279 a 246 c 268 g 257 t

BASE COUNT

ORIGIN

alignment_scores:

Quality: 189.50 Length: 200

Ratio: 1.648 Gaps: 6

Percent Similarity: 57.500 Percent Identity: 29.500

alignment_block:

US-09-438-185-1047 x BF788142

Align seq 1/1 to: BF788142 from: 1 to: 1050

104 ArgAnLeuTtp.....TyrArgLeuLeuSerSerArgPheSerLe 117

45 AGGAGACCTGGGAACGGTCTTCAGGACTCTGAAGCCCTGTATAAAC 94

117 utrPlySerTyrCysProArgPhePheLeuAspTyrLeuGlulAlaphe. 133

95 ACATGCTGCTACGAGCAGACACCATCTCCCTCTTCGGAAAGTACT 144

134 ..GlyLeuLeuSerAspPheLeuAspHis...GlnAlaValIleLysPhe 148

145 GCGGTTTCCTGGAAGACACATCCCGAGCTGGAGATGTTCTCAGATT 194

149 pheGlulLeuGlulHisPheSerTyrTyrProValSerGlyPheValAl 165

195 CTCAGACTGTACTGTTTCCGCTCCCTGCTGTGTCGCTTACTGTC 244

165 aprHisGlnTyrLeuSerLeuLeuGlnAspArgTyrPhePheIleAlas 182

245 GTCTCGAGATTTCTGGGGGCTCCGCTCCGCTCCGCTCCGCTCCGCT 294

182 erValMetArgThrLeuAspLysAspAspPheSerLeuThrProAspLeu 198

295 AGTACATAGCATGATGATGATGATGATGATGATGATGATGATGATG 344

199 IleHisAspLeuLeuGlyHisValProTyrPheLeuHisProSerPhe 215

345 TGTATGAACCTCTGGGACATGTCCTCTCTCTCTCTCTCTCTCTCTCT 394

215 rGlulPhePheIleAsnMetGlyArgLeuPheThrLysValIleGluLys 232

395 CCAGTTTCTCAGGAATGGG

232 aIgluAlaLeuProSerLysGlnArgIleGlnThrLeuGlnSerAsn 248

418 TTGATCGCTGGGGGCGCTGATGATGATGATGATGATGATGATGATGAT 464

249 LeuIleAlaIleValArgCysPheTrpPheThrValGluSerGlyLeu 265

465ATTACTGGTTTACTGTGGAGCTGGGCTTTG 496

265 eGlu.AsnHisGluGlyArgLysAlaTyrGlyAlaValIleSerSer 281

497 CAAGAACCGAGATTCTATAGGAGCATATGCTGGGCTCTTGTATCC 546

282 ProGluLeuGlyHisAlaPheIleAspAsnValArgValLeuPro 297

547 TTGAGCAATTCAGTACTGTTTATCAGACCAAGCAAGCTCTCTGCC 594

seq_name: gb_est13:AA880857

seq_documentation_block:

AA880857 592 bp mRNA EST 26-MAR-1998

LOCUS vx46f08.r1 Stragatene mouse lung 937302 Mus musculus CDNA clone

DEFINITION IMAGE:1278279 5' similar to gb:K03020 PHENYLANINE-4-HYDROXYLASE

(HUMAN); gb:X51942 Mouse mRNA for phenylalanine hydroxylase (MOUSE

); mRNA sequence.

ACCESSION AA880857

VERSION AA880857.1 GI:29898840

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 592)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucab, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMNI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMNI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:670079

Seq primer: -28m13 rev1 ET from Amersham

High quality sequence stop: 430.

Location/Qualifiers

1.organism="Mus musculus"

/strain="C57BL/6 x CBA"

/db_xref="taxon:10090"

/clone_image="IMAGE:1278279"

/clone_lib="Stragatene mouse lung 937302"

/sex="female"

/tissue_type="lung"

/dev_stage="6-8 month old"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: lung; Vector: pBluescript SK-; Site: 1: EcoRI

; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo

dT. 6-8 month old female lung and 1.5 year old male lung

were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP

XR Vector: -5' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'

adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'

136 a 143 c 142 g 167 t

BASE COUNT

ORIGIN

Thu Jul 5 11:24:06 2001

```

alignment_scores:
  Quality: 184.50      Length: 198
  Ratio: 1.577        Gaps: 6
  Percent Similarity: 59.091  Percent Identity: 29.293

alignment_block:
US-09-438-185-1047 x AA880857

Align seg 1/1 to: AA880857 from: 1 to: 592

108 TyrArgLeuLeuSerSerArgPheLeuThrLysSerTyrCysProAr 124
5 TTCAGAGTCTGTAACACCTTGATATAACACATCGCTGCTACGACACAA 54
124 qPhePheLeuAspTyrLeuGluAlaPhe...GlyLeuLeuSerAspPheL 140
55 CCACATCTCCCTCTCTGGAAGTACTGCGGTTTCCGTGAAGACAACA 104
140 euAspHis...GlnAlaValIleLysPhePheGluLeuGluThrHisPhe 155
105 TCCCGCAGCTGGAAGATGTTCTCAGTTTCTGCAGACTTGTACTGTTTC 154
156 SerTyrTyrProValSerGlyPheValAlaProHisGlnTyrLeuSerLe 172
155 CGCTCCGCTCTGTTGCTGCTACTGCTGCTCGAGATTCTTGGGTGG 204
172 uLeuGlnAspArgTyrPheProIleAlaSerValMetArgThrLeuAspL 189
205 CCTGGCATTCGAGTCTTCCACTGCACACAGTACATAGCATGGATCTA 254
189 ysAspAsnPheSerLeuThrProAspLeuIleHisAspLeuGlyHis 205
255 AGCCCATGTACACACCTGACCTGATATCTCATGACTCTTGGGACAT 304
206 ValProThrLeuLeuHisProSerPheSerGluPhePheIleAsnMetGl 222
305 GTGCCCTTTGTTTCAGATPAGAAGCTTTGCCAGTTTCTCAGGAATGG 354
222 yArgLeuPheThrLysValIleGluLysValGlnAlaLeuProSerLysL 239
355 G.....CTGGCATCGCTGGGGCACCTG 377
239 ysGlnArgIleGlnThrLeuGlnSerAsnLeuIleAlaIleValArgCys 255
378 ATGAGTACATTGAGAACTGGCCACA.....ATT 406
356 PheTrpPheThrValGluSerGlyLeuIleGluAsnHisGluGlyArgLy 272
407 TACTGTTTACTGTGGAGTTGGGCTTTGCAAGGAAGAGATCTATAAA 456
272 sAlaTyrGlyAlaValLeuIleSerSerProGlnGluLeuGlyHisAla. 288
457 GGCATATGGTGTGCTGCTCTTCTCATCTTTGGAGAATACAGT...ACTG 503
289 PheIleAsnValArgValLeuProLeuGluLeuAspGln 302
504 TTATTCAGACCAAGCCCAAGTCTGCCNTGGAGCTAGAGAAG 545

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